

SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS RELATING TO THE
PHARMACOGENETICS OF DIFFERENT GENE VARIANTS

<130> ARCD:405US

<140> UNKNOWN

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<210> 1

<211> 4868

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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 Leu His Val Tyr Lys Ser Arg Thr Lys Arg Ser Ser Thr Thr Lys Leu
 50 55 60
 Tyr Leu Ala Lys Gln Val Phe Val Gly Phe Leu Leu Ile Leu Ala Ala
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 85 90 95
 Pro Ala Val Arg Tyr Thr Asn Pro Ser Leu Tyr Leu Gly Thr Trp Leu
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Tyr	Lys	Lys	Ala	Leu	Thr	Leu	Ser	Asn	Leu	Ala	Arg	Lys	Glu	Tyr	Thr
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Ala	Gly	Val</													

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Ser	Thr	Glu	Arg	Leu	Glu	Lys	Tyr	Leu	Gly	Gly	Asp	Asp	Leu	Asp	Thr						
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Cys	Ala	Leu	Leu	Pro	Asp	Leu	Glu	Met	Leu	Pro	Gly	Gly	Asp	Leu	Ala						
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 His Lys Gln Leu Leu Asn Asn Ile Leu Arg Ala Pro Met Arg Phe Phe
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 1075 1080 1085
 Ser Thr Val Asp Asp Thr Leu Pro Gln Ser Leu Arg Ser Trp Ile Thr
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 1105 1110 1115 1120
 Pro Val Phe Thr Ile Ile Val Ile Pro Leu Gly Ile Ile Tyr Val Ser
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 Gly Leu Ser His Glu Val Thr Glu Ala Gly Gly Asn Leu Ser Ile Gly
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 Gln Arg Gln Leu Leu Cys Leu Gly Arg Ala Leu Leu Arg Lys Ser Lys
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Met Val Leu Asp Asn Gly Lys Ile Ile Glu Cys Gly Ser Pro Glu Glu		
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<213> Homo sapiens

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acctttgtgg actgacagct ttttatagtc acgtgacaca gtcaaacatt aacttggtgt 420
atcgattggg ttttgccata tatatatata taagtaggag agggcggaacc tctggcagga 480
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<212> DNA

<213> Homo sapiens

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ttaatttttg gaaaagaagc ctaacttggt cactacatag tcgtccttct tcctctctgg 180
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tctatatttc aatc atg gac caa aat caa cat ttg aat aaa aca gca gag 170
Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu
1 5 10

gca caa cct tca gag aat aag aaa aca aga tac tgc aat gga ttg aag 218
Ala Gln Pro Ser Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys
15 20 25

atg ttc ttg gca gct ctg tca ctc agc ttt att gct aag aca cta ggt 266
Met Phe Leu Ala Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly
30 35 40

gca att att atg aaa agt tcc atc att cat ata gaa cgg aga ttt gag 314
Ala Ile Ile Met Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu
45 50 55 60

ata tcc tct tct ctt gtt ggt ttt att gac gga agc ttt gaa att gga 362
Ile Ser Ser Ser Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly
65 70 75

aat ttg ctt gtg att gta ttt gtg agt tac ttt gga tcc aaa cta cat 410
Asn Leu Leu Val Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His
80 85 90

aga cca aag tta att gga atc ggt tgt ttc att atg gga att gga ggt 458
Arg Pro Lys Leu Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly
95 100 105

gtt ttg act gct ttg cca cat ttc ttc atg gga tat tac agg tat tct 506
Val Leu Thr Ala Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser
110 115 120

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Lys Glu Thr Asn Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser
125 130 135 140

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Thr Cys Leu Ile Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu
145 150 155

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Ile Val Gly Lys Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile
160 165 170

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Tyr Val Phe Met Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile
175 180 185

gta cca ttg ggg ctt tct tac att gat gat ttc gct aaa gaa gga cat 746
Val Pro Leu Gly Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His
190 195 200

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Ser Ser Leu Tyr Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro	
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225 230 235	
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Ile Gly Tyr Val Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser	
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Arg Trp Val Gly Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe	
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Lys Pro Gln Lys Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu	
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Thr Asn Asp Glu Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys	
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Asn Ile Thr Lys Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile	
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Val Ser Ser Tyr Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu	
350 355 360	
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Gln Gln Tyr Gly Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val	
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Phe Thr Ala Val Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile	
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Phe Ser Arg Val Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser	
625 630 635	
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